

02834288 - 041304
CAGCTACATGCCAGGAATCTGGAAAGGAAACGGGAGGGAGCCACCATGCAAACAAACCCAGAGCTCTGCC
CGGCAGCCCCCAGATCTGGGATGCTGGAGGCCATCTATGCAAGGGAGAGATCAACTTCCGAGGG
CTGGGAGAGAGGCCAGTTGAGGTGCAAGCAGTGTGGCCCTCTCGTCTTTGAACTCCT
CTCACCGAGTGGCACCTGCAGCCCCAACCTGGTGTCTCTGGTGGAGGAAAGACCTTGGCTAT
GAAGTCGTGGCTTCTGGATGTCCTGCCAAGGGCTGGTGAAGGAGCAGAGCACAGGTGCCATGGATCC
TGACCAAGTGCCTCCACCTGGGCTGGCCATGGACAAGCTGTACGTGATCACTCTGGCTAGC
ACATCCACCAAGATCCGTAGTGGCATGGAAATGGCTCTCTGGATGCAATCTCACCGTCAACTTC
AGATGGTGTCCACCAAGGAGGATACTCCCATCCACTACCCAGCAGATGAGGGCAACATTCAAGGGACCCC
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GGGCTGAGAGGCTGAGCTGGAGCACATCTCAGAGGACAGGTATGGGGACCC
CTGCATCCAGTACCTGCTTGCCTGGTCAATGGTCAAGGGCAACCCCTAGAGGAGATTCCAGGG
CATGGAGCAGGCTGCCCATGGCTGATCCTGCCAGGTTCTGGCATGGTGTACTCGCTGCCCTG
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TTCTCTTGGGAAAGCCATTGACACTGACAGAGGCTGTTACAGAACATTTGTCACACCCCCACCTGCTCA
CACTATATGACTTCGAGCAGGAGGTGCGAGGACCTGGACACTGTCATCTCAAGGCACTTGTGAAAGCC
TGCAAGGCCACAGCCAGAAGGCCAAGACTACCTAGATGAGCTCAAGTGTAGCAGTGGCCTGGGATCGCGT
GGACATTGCAAGAGTGAATCTCAATGGGACGTGGAATGGAGTCTGTGACTTGGAAAGAGGTGATGA
CHAGTCCCCCTGAGGAAACAGCTGACTTTGTCGCTCTTGTGAGCAGCGTGTGACATGGCGAG
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CAGACCTGGCCCATCGAGTTTGGGACATCAACCTCCCCACTCCAGCAGCCCCAAGAAATGGTCT
TCAAGGGCTTGTACAGATCACTCTGGACATCCCTCTTAAAGAGAATGAAACTCATGTTGGCATCT
ATTCCGGAGCCTCAAGATCTCTCAGGAGGGCAAGATTTCTATGTCCTCAACTAAAGCTTCACTGGC
TTGGACTGGACAGCTGGATCTGGCAAGTCTACATAGGAGACCCATGCTGGATGGGGCTATTAGGTC
TAACCCCTGCTTACCTGAGTCTAAGAAGGCCACCTCTAAACACTAGGTTCTTGTGACCCCTGAC
CCACTCATTAGCTGACCAAGCTCTAGAGGGCAGGAGCTCAGATCTATTGTAATTACCTCCATCTTCA
CCCACAGCATTATCTGCTGATCATTCTGGCAGAAACCCCAAGATATTGCTCAAGGGTACCCAAATGCTACT
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AAAAAAAAAAAAAAAAAAAAAA

Figure 1
(Sheet 1 of 17)

AP32911

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KGLVKHAQSTGAWILTEALHVGGLAHVGCAVADHSLAESTETK1KVVAJGMAS1D11HKQ11DGVHOKEDTP1HYPADEGN1QGPLCP1
ESNLSHF11VEFGALGSGNDG1TE1Q1S1EKH1S00RTGYGGTSC1Q1F1V1CLVNGDPNTLER1S1RAVEQAAAPW1LAGSGG1ADVLA
ALVSGPHLLVHQVAKOFREKFFSECFSEWA1VHWTELLQ1AAH1HLLTVYDFE0EGSE1D1DTV1LKA1LVKACKSHS0EAQDYLDELY
LAVAWDKVIJAKSEJFNGDVEWKSCD111EVMTDALVENKFDFV1LFD1SGADMAEFLTYG1LQCLYHSVSFKSLLFELLORKHEEGRL1
EAGLGAQOQAKELP1GL1AFSLHVS1V1KDF1HDAC1GFYQDGR1MEE1G1PK11GOKWLFD1EKKSED1PWRD1FL1WAVLQ1NRYEMATY
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E1DCVGCAF1TK1WWG1M1TGTP1L111GAFT1F111YT1N11SF1SED1P1Q1MD1E1D1Q1F1D1M1E1K1C1S1F1C1S1F1C1S1F1C1
E1Q1A1F1L1T1W1K1F1W1G1A1F1V1F1G1N1V1V1M1Y1A1F1F1L1F1T1Y1V1L1V1D1F1F1P1P1Q1G1S1C1S1E1V1L1E11
E1D1N1W1N1K1C1M1V1A1F1F1V1G1V1T1C1M1V1P1S1V1F1A1G1T1V1L1J1H1F1A1H1K1Q1G1F1K111V1E1R1Q1G1F1T1D1E1D1T1H1V1
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E1C1V1V1Q1G1N1A1M1F1W1K1F1Q1Y1H1L1J1V1E1Y1H1G1R1P1A1F1F1L1S1H1S1V1L1K1Q1V1F1K1A1Q1H1R1Q1H1L1E1D1Q1K111T1W1E1T1V1
E1C1S1E1G1E1V1R1K1T1A1H1V1D1L1J1A1K1Y1J1G1L1R1E1Q1E1K1J1K1C1E1S1C1A1N1C1L1S1S1M1D1T1A1P1G1T1Y1S1S1Q1P1A1D1R1E1Y1L1S1
E1C1S1E1G1E1V1R1K1T1A1H1V1D1L1J1A1K1Y1J1G1L1R1E1Q1E1K1J1K1C1E1S1C1A1N1C1L1S1S1M1D1T1A1P1G1T1Y1S1S1Q1P1A1D1R1E1Y1L1S1

Figure 2
(Sheet 2 of 17)
AP32911

Human TFR nucleotide sequence

SEQ New: 3498 bp

Composition: 634 A; 1089 C; 1143 G; 632 T; 0 OTHER

Percentage: 18% A; 31% C; 33% G; 18% T; 0% OTHER

Molecular weight (kDa): ssDNA: 1081.34 dsDNA: 2157.1

ORIGIN

1 ATGCAGGATG TCCAAGGCC CCGTCCCGGA AGCCCCGGGG ATGCTGAAGA CCGGCGGGAC
 61 C1GGGCTTGC ACAGGGGGCGA GGTCAACTT GGAGGGTCTG GGAAGAAGCG AGGCAAGTT
 121 GTACGGCTGC CGAGCGGAGT GGGCCCGCT GTGCTCTTTC ACCTGCTGCT TGCTGAGTGG
 181 CACCTGCCGG CCCCCAACCT GGTGGTGTCC CTGGTGGGTG AGGAGCAGCC TTTGCCATG
 241 AAATCCGGC TCGGGATGT GCTGGCGAAG GGGCTGGTCA AGGCAGGCTCA GAGCACAGGA
 301 GCCTGGATCC TGACCACTGTC CCTCCCGCTG GGCCTGGCCCA GGCATGTCGG GCAGGCCGTC
 361 CGCGACCACT CGCTGGCCAG CACGTCCACC AAGGTCCCTG TGTTGCTGT CGGCATGGC
 421 TCGCTCCGCC GCCTCCTGCA CCGCCFCATT CTGGAGGAGG CCCAGGAGGA TTTTCCCTGTC
 481 CACTACCCCTG AGGATGACGG CGGCAGCCAG GGGCCCCCTCT GTTCACTGGA CAGCAACCTC
 541 TCCCACCTCA TCCCTGGTGGA GCCAGGGCCC CCGGGGAGG GGCATGGGCT GACGGAGCTC
 601 CGGGCTGAGGC TGGAGAAGCA CATCTGGAG CAGAGGGCGG GCTACGGGGG CACTGGCAGC
 661 ATCGAGATCC CTGTCCTCTG CTTGCTGGTC AATGGTGTATC CCAACACCTT GGAGAGGATC
 721 TCCAGGGCCG TGGAGCAGGC TGCCCCGTGG CTGATCCTGG TAGGCTCGGG GGGCATCGCC
 781 GATGTCCTTG CTGCCCTAGT GAAACAGCCC CACCTCTGG TGCCCCAAGCT GGGCGAGAAC
 841 CAATTAGG AGAAGTCCCC CAGCAAGCAT TTCTCTTGGG AGGACATCGT GCGCTGGAC
 901 AAGCTCTGC AGAACATCAC CTCACACCCAG CACCTGCTCA CCGTGTATGA CTTCGAGCAG
 961 GAGGGCTCCG AGGAGCTGGA CACGGTCATC CTGAAGGCGC TGGTAAAGC CTGCAAGAGC
 1021 CACAGCCAGG AGCCTCAGGA CTATCTGGAT GAGCTCAAGC TGGCCGTGGC CTGGGACCGC
 1081 GTGGACATCG CCAAGAGTGA GATCTTCAAT GGGGACGTGG AGTGGAAAGTC CTGTGACCTC
 1141 GAGGAGGTGA TGGTGGACGC CCTGGTCAGC AACAAAGCCCG AGTTTGTCGCG CCTCTTTGTC
 1201 GACACCGGCG CAGACGTGGC CGACTTCTTG ACCTATGGGC GGCTGCAGGA GCTCTACCGC
 1261 TCCCTGTCAC GCAAGAGCC GCTCTTCGAC CTGCTGCAGC GGAAGCAGGA GGAGGCCC
 1321 CTGACGCTGG CGGGCCTGGG CACCCAGCAG GCCCCGGGAGC CACCCCGGGG GCCACCGGGC
 1381 TTCTCCCTGC ACGAGGTCTC CCGCCTACTC AAGGACTTCC TGCAGGACGC CTGCGAGGC
 1441 TTCTACCAAGG AGGGCCGGCC AGGGGACCGC AGGAGGGCGG AGAAGGGCCC GGCCAAGC
 1501 CCCACGGGCC AGAAGTGGGT GCTGGACCTG AACCAAGAAGA GCGAGAACCC CTGGCGGGAC
 1561 CTETTCCTGT GGGCCGTGCT GCAGAACCGC CACGAGATGG CCACCTACTT CTGGGCCATC
 1621 GGCCAGGAAG GTGTGGCAGC CGCACTGGCC GCCTGAAAAA TCCTCAAAGA GATGTCGCAC
 1681 CTGGAGACGG AGGCCGAGGC GGCCCCAGCC ACGGCGGAGG CGAAATACGA CGGGCTGGCC
 1741 CTTGACCTCT TCTCCGAGTG CTACAGCAAC AGTGAGGCC GCGCCTTCGC CCTGCTGGT
 1801 CGCCCGAACCC GCTGCTGGAG CAAGACCACC TGCTGCACC TGGCCACCGA GGCTGACGCC
 1861 AAGGCCCTCT TTGCCCCACGA CGGGCTTCAG GCCTTCTGA CCAGGATCTG GTGGGGGGAC
 1921 ATGGCCCGAG GCACGCCCAT CCTGGGGCTG CTAGGAGCCT TCCTCTGCC CGCCCTCGTC
 1981 TATACCAACC TCATCACCTT CAGTGAGGAA GCTCCCCCTGA GGACAGGCCT GGAGGACCTG
 2041 CAGGACCTGG ACAGCCTGGA CACGGAGAAG AGCCCGCTGT ATGGCCTGCA GAGCCGGGTG
 2101 GAGGGAGCTGG TGGAGGGGCC GAGGGCTCAG GGTGACCGAG GCCCCACGTG TGTCTTCCTG
 2161 CTCACACGCT GGGGAAATT CTGGGGCCT CCCGTACTG TGTTCTTGGG GAACTGGTC
 2221 ATGTACTTCG CCTTCCTCTT CCTGTCACCC TACGTCCTGC TGTTGGACTT CAGGCCGCC
 2281 CCCCAGGGGCC CCTCAGGGCC CGAGGTCACT CTCTACTTCT GGGTCTTTAC GCTGGTGTG
 2341 GAGGAATCC GGCAGGGCTT CTTCACAGAC GAGGACACAC ACCTGGTGAA GAAAGTCA
 2401 CTGTATGTGG GGGACAACGT GAACAAGTGT GACATGGTGG CCATCTTCCT GTTCATCGTC
 2461 GGTGTCACCT GCAGGATGCT GCCGTCGGCG TTGAGGCTG GCGCACGGT CCTCGCCATC
 2521 GACTTCATGG TGTTCACGCT GCGGCTGATC CATATCTTG CCATACACAA GCAGCTGGGC
 2581 CCCAAGATCA TCGTGGTAGA GCGCATGATG AAGGACGTCT TCTTCTTCCT CTTCTTCCTG
 2641 AGCGTGTGGC TCGTGGCCTA CGGTGTCACC ACCCAGGCGC TGCTGCACCC CCATGACGGC
 2701 CGCCTGGAGT GGATCTTCCG CGGGGTGCTC TACCGGCCCT ACCTGCAGAT CTTCGGCCAG
 2761 ATCCCACCTGG ACGAGATTGA TGAAGCCCCT GTGAACACTGCT CCACCCACCC ACTGCTGCTG
 2821 GAGGAACCTCAC CATCCTGCC CAGCCTCTAT GCGCAACTGGC TGGTCATCCT CCTGCTGGTC
 2881 ACCTTCTGT TGGTCAACCAA TGTGCTGCTG ATGAACCTGC TCATCGCCAT GTTCAGCTAC
 2941 ACGTTCCAGG TGGTGCAGGG CAACGCAGAC ATGTTCTGGA AGTTCCAGCG CTACAACCTG

Figure 3A
 (Sheet 3 of 17)
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300 ATTCTGGAGT ACCACGAGCG CCCCCGCCCTG GCCCCCGCCCT TCATCCCTGCT CAGCCACCTG
301 AGCCCTGACGC TCCGCCGGGT CTTCAGAGAG GAGGCTGAGC ACAAGCGGGG ACGACCTGGAG
302 AGAGACCTGG CAGACCCCCG CGACCAAGAG GTCCTCACCT GGGAGACAGT CCAGAGAGGAG
303 AACTTCTGA GCGAGATGGG GAGGCCGAGG AGCAGACGCC AGGGGGAGGT GCTGCGGAA
304 ACCGCCACAA GAGTGGACTT CATTGCCAAC TACCTCTGGG GGCTGAGAGA GCAAGAAAAA
305 CGCATCAAGT GTCTGGAGTC ACAGATCAAC TACTGGCTGG TGCTCGTGTC CTCCGTGGC
306 GACGTGCTGG CCCAGGGTGG CGGCCCGCGG AGCCTCTAGC ACTGTGGCGA GGGAGGCCAC
307 CTGGTGGCTG CTGACCACAG AGGTGGTTA GATGGCTGGG AACAAACCGG GGCTGGCCAG
308 CCTCCCTCGG ACACATGA

Figure 3B
(Sheet 4 of 17)
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Human CFF8 protein coding sequence
Translational of Htrpb coding (1-349F)
Universal code
Total amino acid number: 1165, MW=13128.
Max ORF: 1-3495, 1165 AA, MW=13128.

ORIGIN

1 MCDVQGPRPG SPGDAELARE LGLHFGEVNF GGSGKKRGKF VRVPSCVAPS
2 VLFDLILLAEW HLFAPNLVVS LVGEEQFAM KSWLRDVLRK GLVKAAQSTG
3 AWIILTSALRV GLARHVGQAV FDHCLASTST KVRRVAVGMA SLGRVVLHRR
4 LEEAQEDFPV HYPEDDGGSQ GPLCSLDSNL SHFILVEPGP PGKGDGLTEL
5 FLRLEKKHISE QFAGYGGTGS JEIFVLCILV NGDPNTLERJ SRAVEQAAAPW
6 LILVGSGGIA DVLAALVNQF HLLVPKVAEK QFKEKFPSKH FSWEDIVRWI
7 FLLQNITSHQ HLLTVYDFEQ LGSEELDTVJ LKALVKACKS HSQEPQDYLI
8 ELKLAVALWDR VDIAKSEJFN GDVEWKSCDL EEVVMVDALVS NKPEFVRLFV
9 DNGADVADFL TYGRLQELYR SVSRKSELLFD LLQRKQEEAR LTLAGLGTQG
10 AREPPFAGFFA FSLHEVSRVL KDFLQDACRG FYQDGRPGDR RRAEKGPAKK
11 FTGOKWLLDL NQKSENFWRD LFLWAVLQNF HEMATYFWAM GQEGVAAALA
12 ACKJILKEMSH LETEAEAAARA TREAKYERLA LDLFSECYSN SEARAFALLV
13 RANRCWSKTT CLHLATEADA KAFFAHDGVQ AFLTRIWWGD MAAAGTPILRI
14 LGAFLCFLALV YTNLITFSEE AFLKTGLEDL QDLDSDLTEK SPLYGLQSRV
15 EELVEAPRAQ GDRGPRAVFL LTRWRKFWGA PVTVFLGNVV MYFAFLFLFJ
16 YVLLVDFRPP POGPSGFEVN 1YFWVFTLVL EEIROQFFTD EDTHLVKKFT
17 LYVGDNWNKC DMVAJFLFIV GVTCKMLPSA FEAGRTVLAM DFMVFTLRLI
18 H1FAJHKQLG PK11VVERMM KDVFFFLLFFL SVWLVAYGVT TOALLHPHDG
19 F1EWFRRVL YRPYLQ1FGQ 1PLDE1DEAR VNCSTHPLLL EDSPSCPSLY
20 ANWLWJ1LLV TFL1LVTNVLL MNLLIAMFSY TFOVVOQGNAD MFWKFORYNL
21 IVEYHEFPA1 APPF1LLSHL S1T1RRVFKK EAEEHKREHLE RDLPDPPLDQK
22 VVTWETVQKE NFLSKMEKRR RDSEGEVLRK TAHRVDFIAK YLGGLREQEK
23 F1KCLESQIN YCSVLVESVA DVLAQGGGPR SSQHCGEGSQ LVAADHKGGI
24 DGWEQPGAGQ PPSDT*

Figure 4
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FIGURE 1 - COMPARISON OF THE AMINO ACID SEQUENCES OF MOUSE AND HUMAN TEF1

Figure 5
(sheet 6 of 17)

AP329 II

Classification and Secondary Structure Prediction of Membrane Protein

<http://azura.aproteome.bio.tuat.ac.jp/sosui/>

Orientation c: the N-terminus of mTrp8: 11
Number of transmembrane helices of mTrp8: 1
Position of transmembrane helices of mTrp8: helix begin end
1 731 751
2 769 791
3 807 829
4 834 861
5 870 891
6 951 971

Orientation c: the N-terminus of hTrp8: 1N
Number of transmembrane helices of hTrp8: 1
Position of transmembrane helices of hTrp8: helix begin end
1 731 751
2 770 791
3 807 829
4 843 863
5 871 893
6 951 971

Figure 6A
(Sheet 7 of 17)

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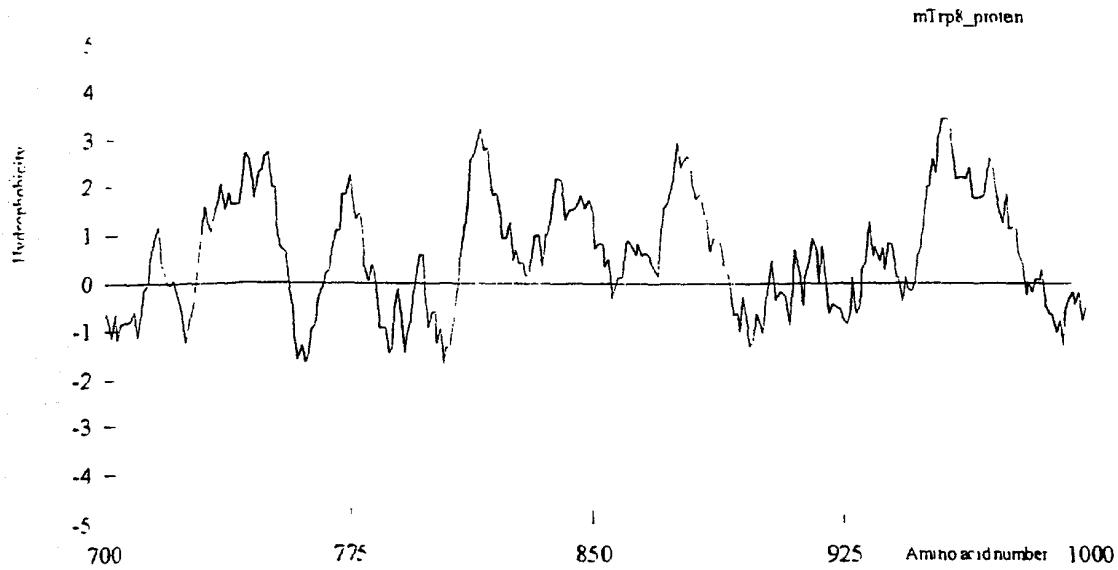
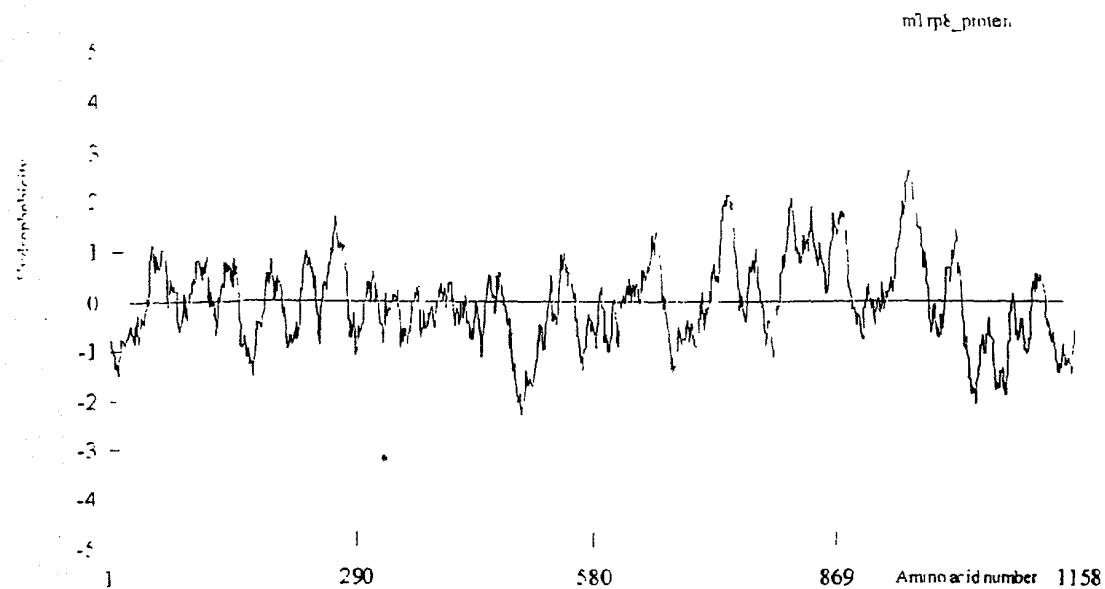


Figure 6B
(Sheet 8 of 17)

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Hydrophobicity profile of hTrpE (Made with DNAMAN software)

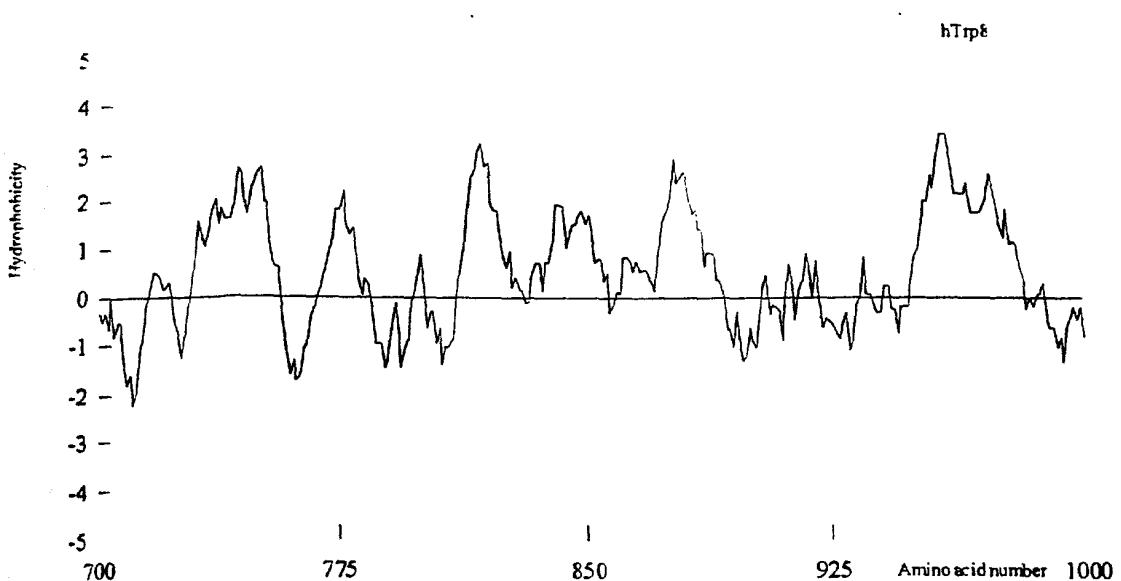
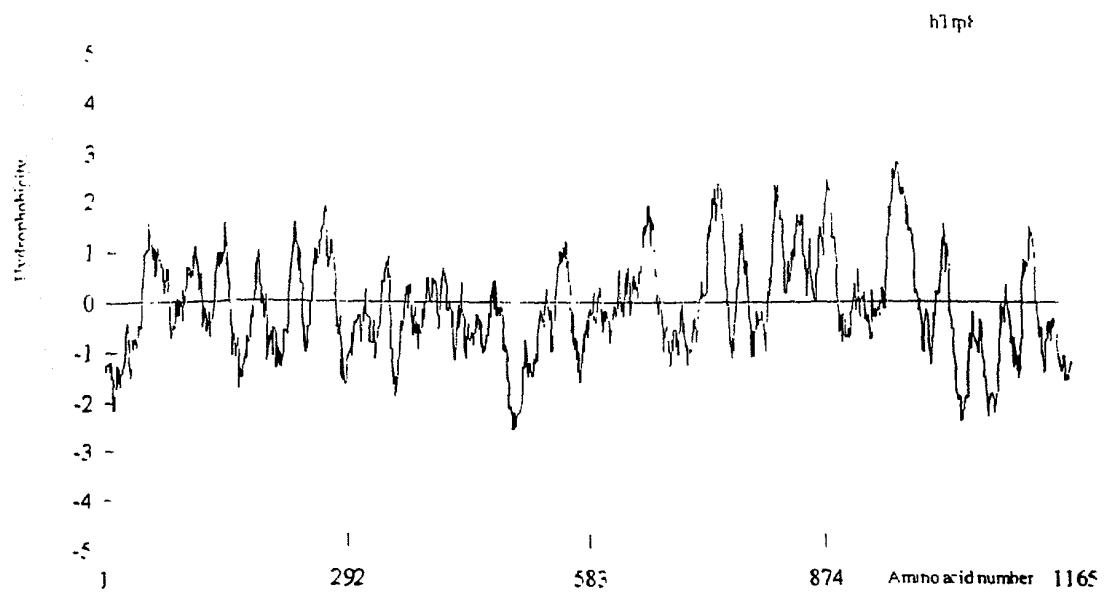


Figure 6C
(Sheet 9 of 17)
AP32911

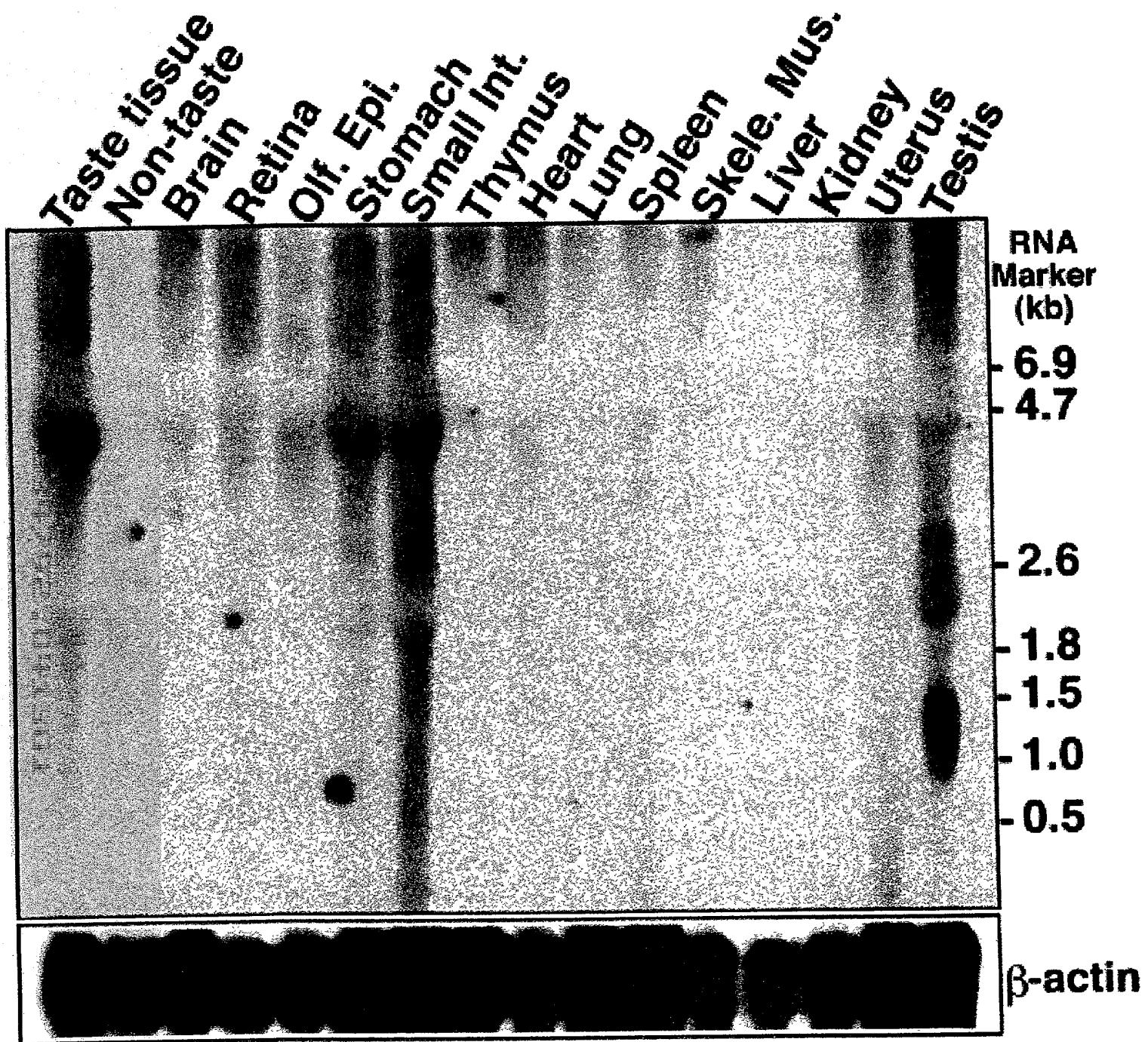


Figure 7
(Sheet 10 of 17)
AP32911

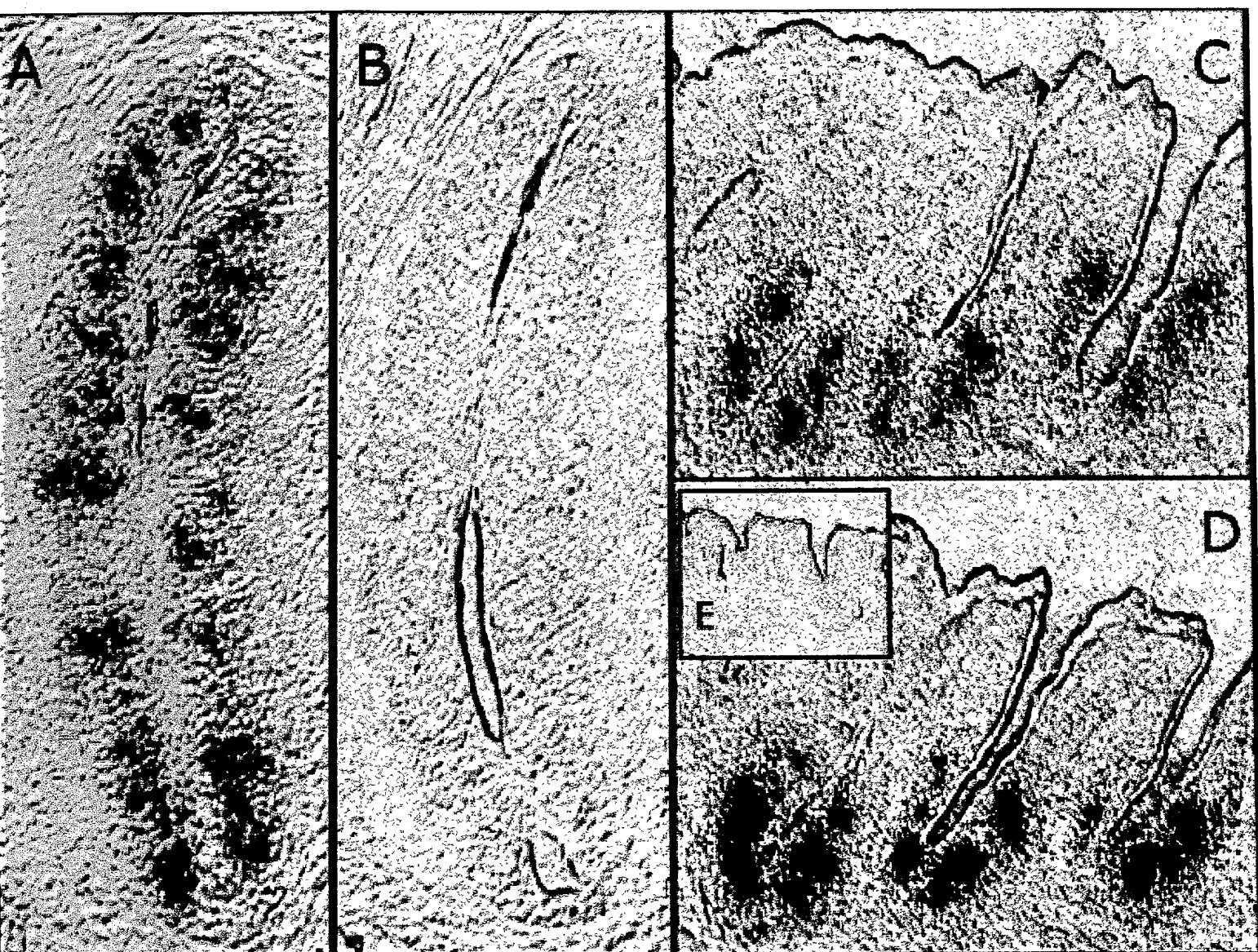


Figure 8
(sheet 11 of 17)
AP32911

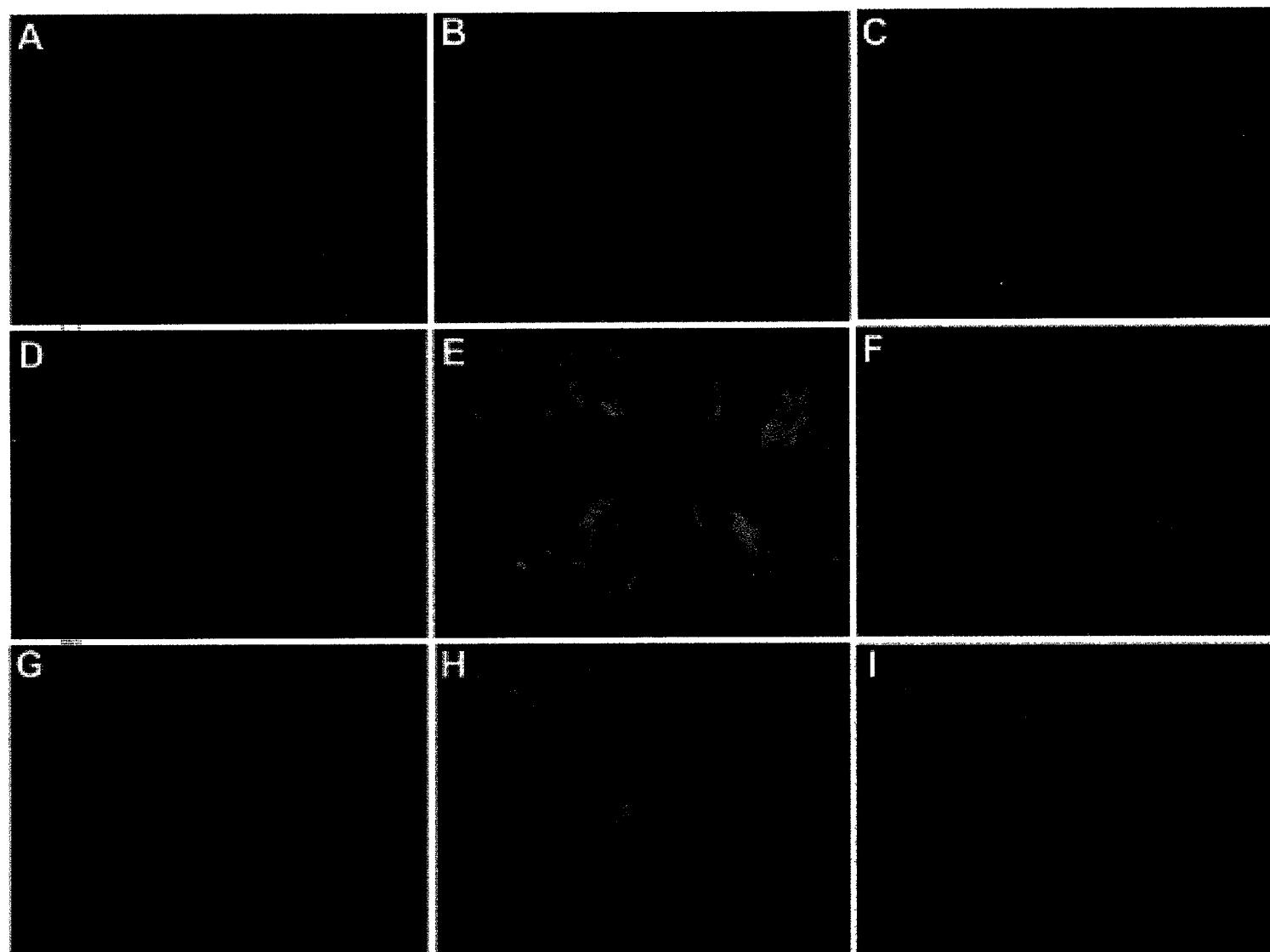


Figure 9
(sheet 12 of 17)
AP32911

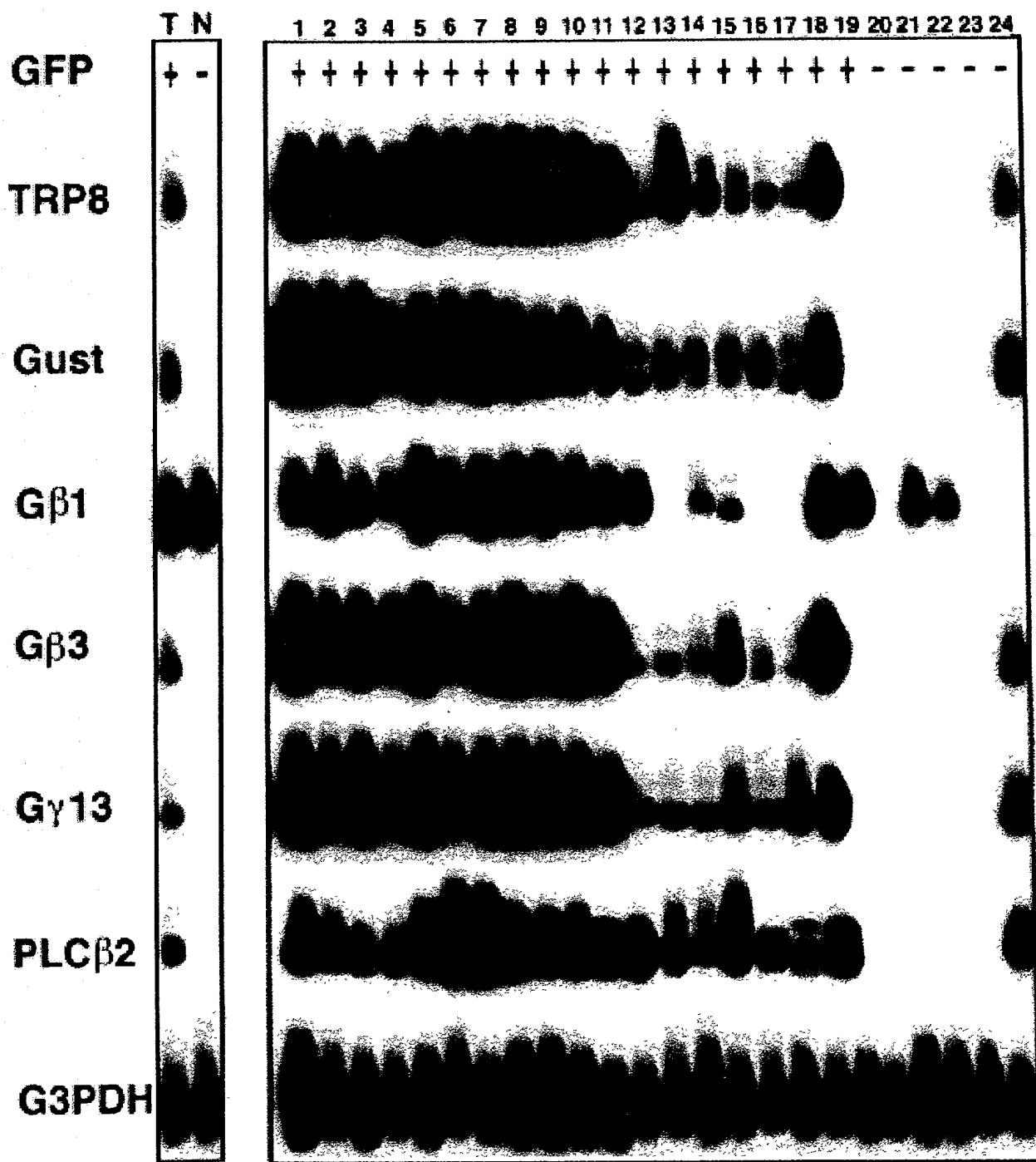


Figure 10
(sheet 13 of 17)
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Taste
Brain

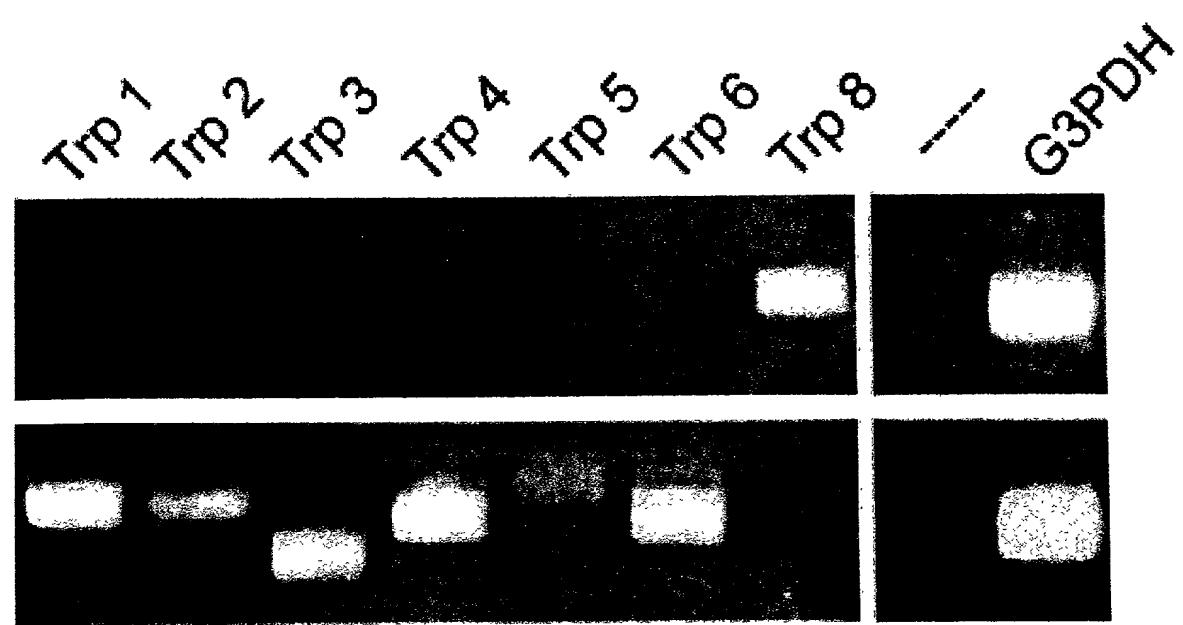
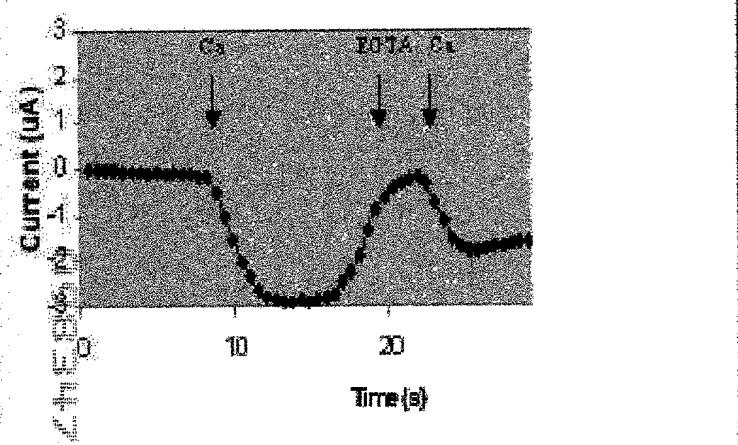
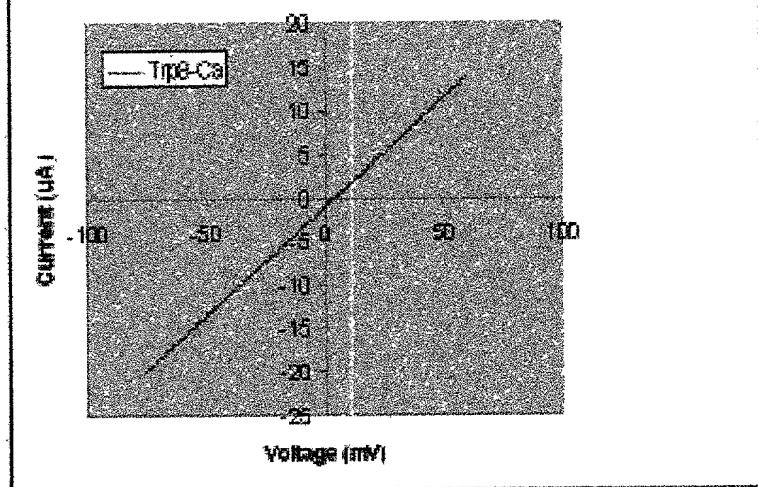


Figure 11
(Sheet 14 of 17)
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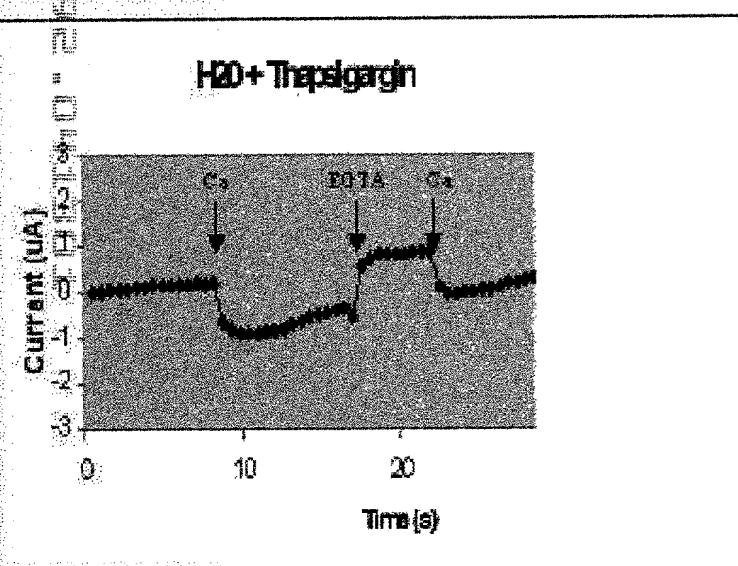
Trp8+Thapsigargin



IV Relationship in Trp8 Injected oocytes



H2O+Thapsigargin



PeakI_{Ca}

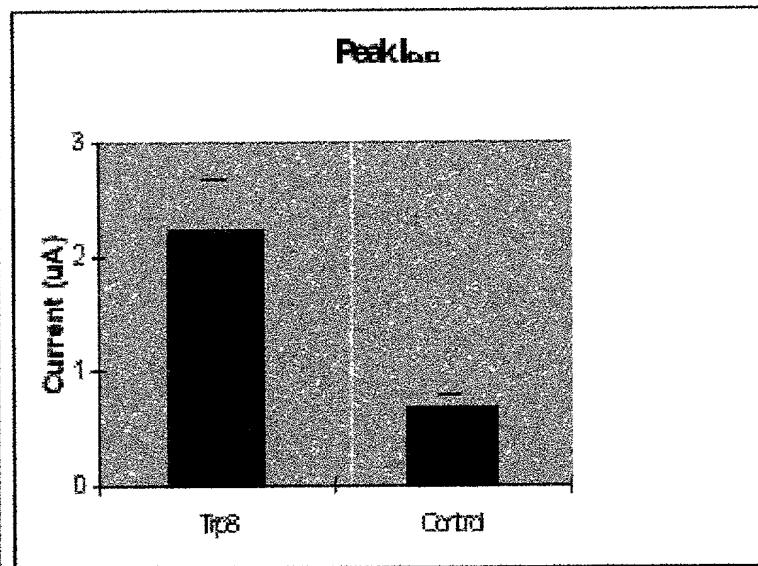


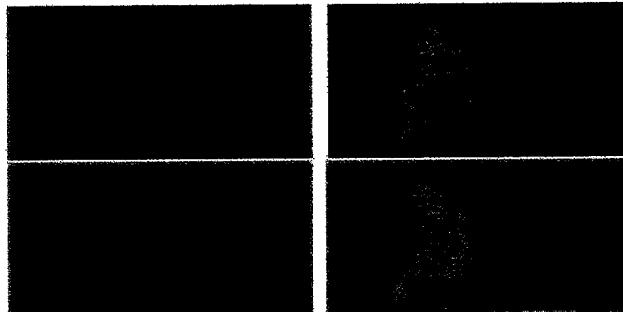
Figure 12
(sheet 15 of 17)

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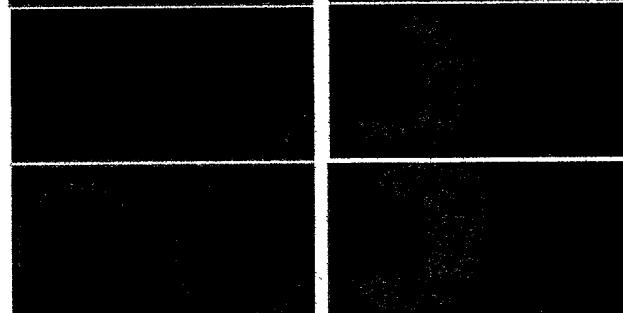
Injected with: **H2O** **TRP8 cRNA**

Thapsigargin 2uM: + - + -

0 s after Ca addition



25 s after Ca addition



50 s after Ca addition



75 s after Ca addition

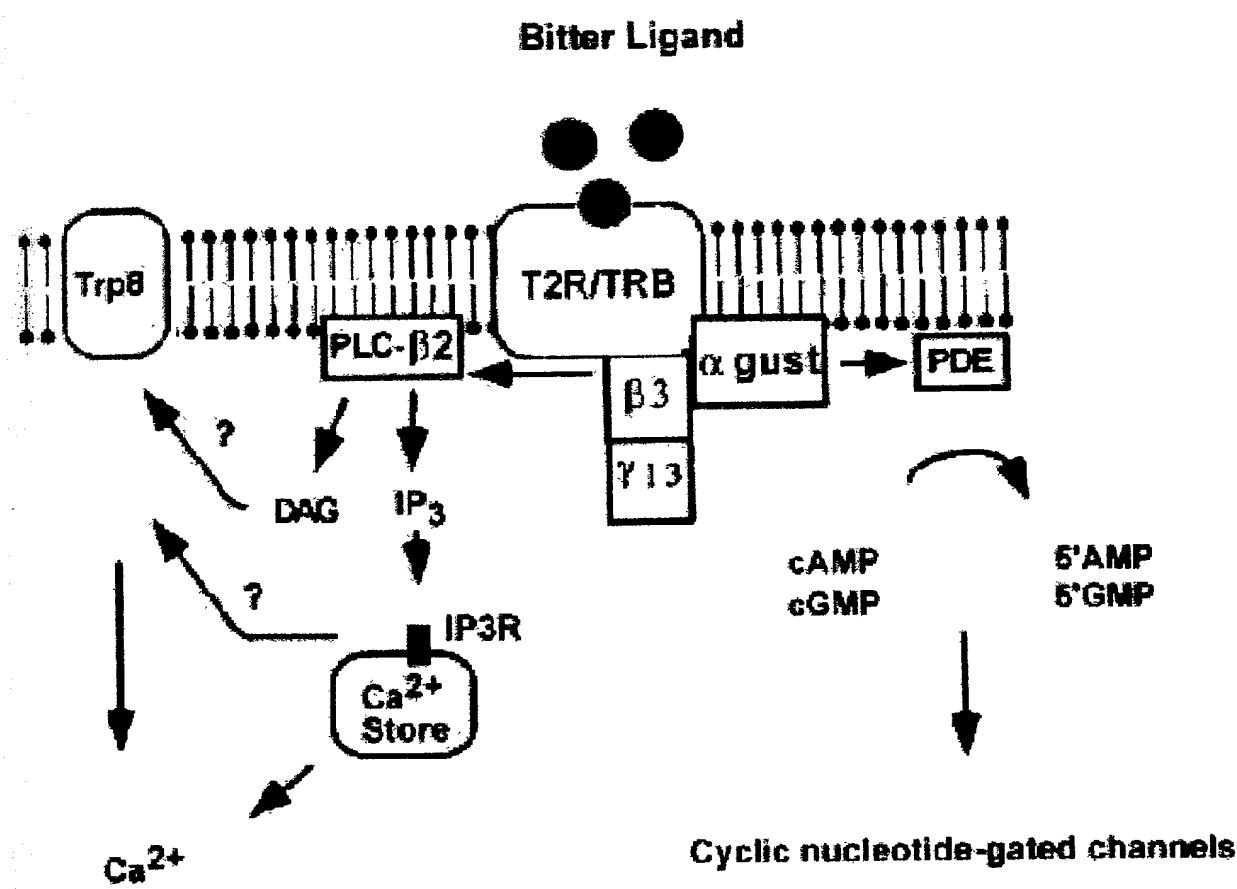


100 s after Ca addition



Figure 13
(Sheet 16 of 17)
A P32911

Transduction of Taste Stimuli



Modified from Kinnamon. *Neuron* (2000) 25:507-510

Figure 14
(Sheet 17 of 17)
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